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FOR IMMEDIATE RELEASE

Replicate Comparison Tool added to GeneMarker®HID software eases Replicate Profile Concordance while providing 40% time savings

August 28, 2013, State College PA 16803 USA SoftGenetics LLC announced the addition of a special replicate comparison tool in its GeneMarkerHID Human Identity Software. Many forensic and paternity labs choose to process multiple replicates of their samples for a variety of reasons. This technique lessens the impact of allele dropout and other common sequencing associated artifacts, allowing analysts to confidently deduce a consensus genotype. Replicates are also commonly used to successfully analyze trace amounts of DNA, in some cases as little as 100pg. Despite these advances, comparing replicates manually can be both time consuming and error prone. For example researchers must often use multiple software packages – one to genotype the data, and a second spreadsheet or statistical program in which to compare samples.

GeneMarkerHID software's Replicate Comparison Tool, developed in collaboration with DNA Diagnostics Center, Fairfield, OH and now available in GeneMarkerHID, automates replicate comparison and is built directly into the program. The analyst simply imports the raw data files (.fsa, .HID), performs genotyping, and then automatically compares profile replicates, all using a single program; eliminating time consuming and error prone data transfer.

Dr. Tricia Frye, Associate Laboratory Director of DDC, indicated "...the new replicate comparison tool will have a tremendous impact on our workflow as we are experiencing a 30-40% analysis time improvement... We are very pleased with the tool and it will add a great deal of efficiency and quality to our process."

Results are automatically displayed in the informative report table. A status column for a specified marker will display a C for Concordant if the replicates have the same call, a D for Discordant, if the call is different, and N, for Null, if only one replicate has allele calls (i.e. the other replicates failed). For C and N calls, the Final Genotype column is automatically filled with the consensus genotype. At discordant (D) markers, the analyst may use their expertise to select the most accurate call from a dropdown menu.

The report table is linked with the actual electropherogram, allowing users to quickly and efficiently analyze markers of interest. GeneMarkerHID also includes relationship testing, database search, and mixture deconvolution applications, allowing analysts to further explore for potentially contaminated samples. Finally, GeneMarkerHID supports numerous reporting and saving options, including customizable print reports, excel and text exports, and automated CODIS formatting.

GeneMarkerHID software is an expert system using modern technologies which increase speed of profile analysis by removal of sequence, PCR and other artifacts. The Windows® software includes relationship testing, mixture deconvolution, and automated database searching modules eliminating the need for other tertiary analysis packages.